

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIHPPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDGGGLVCDGALQGITSWGSDFCGRSDKPGVYTNI CRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGACACGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG
CGCGCCGCCACGCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCCG
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGGCCCGCCCCCGCCCCG
CCCCGCGCGCGGGGAACCGGCGGATTCTCGCGCTCAAACACCTGATCCCATAAAC
ATTATCCTCCCGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCCGCGCCCGCGCCGCCCTCG
CCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGGGAGC
GGAGCGCGCCGAGCTCTGTCGCCGCGCGCGGCCGGGGCCGGGCGTAGCGCGCGCTGGA
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC
CCCCGCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCTTGGCAGGTGGCAGCCCCATGCCAGGTGCCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGCTGCAGGCTGTGCCGTGGGCGATCCCTG
CTGCCAGCCAGCGCATCTTCTGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCCGAACCTCACCATCTGTGGCTGCACTCGAATGTGTGCCCCGAATTGATGC
GGCTGCCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTGCCACATTCACGGCCTGGGCGCCCTACACAGCTGCACCTGGACCGC
TGCGGCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACCGCGCTGCAGGCACTGCCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGCAACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCTTCCGTGGGCTG
CACAGCTCGACCGTCTCTACTGCAACGAGAACCGCGTGGCCCATGTGCAACCGCATGCCCTT
CCGTGACCTTGGCCCGCTCATGACACTCTATCTGTTTGCCAAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCAACCGCTCTGGGCTTGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA
GGTCCCTGCAGCTCCCGCAACGCTTGCTGGCCGTGACCTCAAACGCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGTGTCAGCCAGATGCCGCTGACAAGGCCCTCAGT
ACTGGAGCCTGGAAGACAGCTTTCGCGAGGCAATGCGCTGAAGGGACGCGTGCCGCCGGTG
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACAGGGTT
CCCCACCTCGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGACGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACTGCAGCTCACCCTTGGGCTGGCGCTGGTGCTGTGGAGACTGCT
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCTTCCGCCCGCCACCCCATCTCCACCCATCATGTTTACAGGG
TTCGGCGCAGCGTTTTGTTCCAGAACGCGCCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAATAATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA
AAAA

09978295-101501

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNRISHVPAASFRACRNLITLWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRHLTHLDRCLQELGPGLFRLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRLHSLDRLLHQNVRVAHVHPHAFRDLGRIMTYLFLANNLSALPTEALAP
LRALQYLRINDNPWVCDRCRARPLWAWLQKFRGSSSEVPKSLPQRLAGRDLEKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

007605-10101